

Effect of Kudzu-foxglove supplementation on serum and urine ^1H NMR-based metabolomics in ovariectomized rats fed with a high-fat diet

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1. Introduction

Consumption of Kudzu root and foxglove (PR) has been associated with several health benefits; however, their holistic metabolic changes are not adequately understood. The aim of current study was to investigate the metabolic changes associated with PR supplementation in serum and urine metabolic signatures on ovariectomized/high-fat diet (HFD) rat model.

2. Approach

Female Sprague-Dawley rats were OVX at age 8 weeks. After one-week of recovery, rats were randomly divided into six groups to receive vehicle, PR, or 17β -estradiol (ES) and maintained on a HFD. Then, each group was further divided into two subgroups for no exercise (C, PR, and ES) or exercise treatment (C-Ex, PR-Ex, ES-Ex). The PR, 17β -estradiol, or vehicle were treated for 8 weeks. The serum and urine metabolome were examined using ^1H NMR. Multivariate statistical approaches, such as orthogonal projection to latent structures squares-discriminant analysis were built to evaluate the PR effects.

4. Discussion

To our knowledge, this study is the first to address the molecular mechanism of PR from a metabolomics perspective. The study showed a systemic metabolic response in serum and urine metabolomics to PR supplementation in ovariectomized/high-fat diet rat. The present study demonstrates that serum and urine metabolomics method could be a potentially useful tool to understand the metabolic effect and the mechanism from a systematic view.

References

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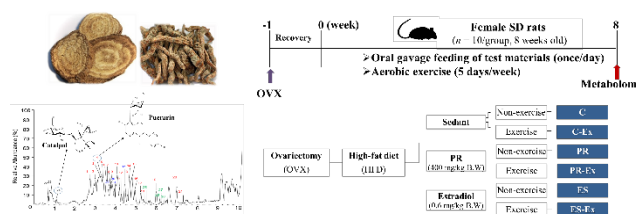


Figure. Study design

3. Results

From the 37 identified metabolites, 8 were significantly changed in the serum and from 74 identified metabolites, 23 were significantly changed in the urine. These serum metabolites are commonly involved in caffeine metabolism; nitrogen metabolism; aminoacyl-tRNA biosynthesis; histidine metabolism; glycolysis or gluconeogenesis; TCA cycle; glyoxylate and dicarboxylate metabolism. These urine metabolites are involved in arginine and proline metabolism; aminoacyl-tRNA biosynthesis; D-Glutamine and D-glutamate metabolism; nitrogen metabolism; valine, leucine and isoleucine degradation; glycine, serine and threonine metabolism.